

## SEQUENCE LISTING

<110> Taylor, Alexander H

<120> Monoclonal Antibodies with Reduced  
Immunogenicity

<130> P50770

<150> 60/083,367

<151> 1998-04-28

<160> 97

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 429

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(429)

<400> 1

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1 5 10 15

gtc ctg tcc cag gtg cag ttg cag gag tcg ggc cca gga ctg gtg aag 96

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys

20 25 30

cct tca cag acc ttg tcc ctg acc tgc gct gtg tct ggt ggc tcc atc 144

Pro Ser Gln Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35

40

45

act agt gct tac tac tat tgg agc tgg atc cgc cag tca cca ggg aag 192  
 Thr Ser Ala Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys

50

55

60

gga ctg gag tgg att ggg agt atc tat tat agt ggg acc att ttc tcc 240  
 Gly Leu Glu Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser  
 65 70 75 80

aac cca tcc ctc aag agt cga gtc gcc atg tca gta ggc acg tcc aag 288  
 Asn Pro Ser Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys  
 85 90 95

acc cag ttc tcc ctg agc ttg agt tct gtg acc gcc gcg gac acg gcc 336  
 Thr Gln Phe Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110

gtg tac tac tgt gcg aga ggt ctg ctc ctc acc att gga ctg acc aac 384  
 Val Tyr Tyr Cys Ala Arg Gly Leu Leu Leu Thr Ile Gly Leu Thr Asn  
 115 120 125

tac tac ttt gac tac tgg ggc ccg gga acc ctg gtc acc gtc ttc 429  
 Tyr Tyr Phe Asp Tyr Trp Gly Pro Gly Thr Leu Val Thr Val Phe  
 130 135 140

&lt;210&gt; 2

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(414)

&lt;400&gt; 2

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag cta cag gag tcg ggc cca gga cta gtg aag	96
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys	
20 25 30	
ccg tca cag acc ctg tcc ctc acc tgc ggt gtc tct ggt gcc tcc atc	144
Pro Ser Gln Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile	
35 40 45	
aat agt ggt gtt cat tac tgg gcc tgg ata cgc cag cct gca gga aag	192
Asn Ser Gly Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys	
50 55 60	
gga ctg gag tgg att ggc aat atc tat cat agt ggg agc gcc tac tac	240
Gly Leu Glu Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr	
65 70 75 80	
act cca tcc ctc gag agt cga gtc tcc atg tca ata gag acg tcc aag	288
Thr Pro Ser Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys	
85 90 95	
agc cag ttc ttc cta aac tta aat tct ctg acc gcc gcg gac acg gct	336
Ser Gln Phe Phe Leu Asn Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala	
100 105 110	
atc tat tat tgt gcg aga cga cat act tcg tca gac tac ttt gac ttt	384
Ile Tyr Tyr Cys Ala Arg Arg His Thr Ser Ser Asp Tyr Phe Asp Phe	
115 120 125	
tgg ggc cgc gga atc ctg gtc atc gtc tcc	414
Trp Gly Arg Gly Ile Leu Val Ile Val Ser	
130 135	

<210> 3  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1)...(427)

<400> 3

atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc gaa gga 48  
 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Glu Gly  
 1 5 10 15

gtc cgt gca gac gtg cag ctg gtg cag tcc gga gca gag gtg aaa aag 96  
 Val Arg Ala Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

ccc ggg gag tct ctg aag atc tcc tgt aag gtc tct gga aat gaa ttt 144  
 Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe  
 35 40 45

acc aac tac tgg atc gcc tgg gtg cgc cag atg tcc ggg aaa ggc ctg 192  
 Thr Asn Tyr Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu  
 50 55 60

gag tgg atg ggg agc atc tat cct ggt gac tct gat acc aga tac aac 240  
 Glu Trp Met Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn  
 65 70 75 80

ccg tcc ttc caa ggc caa gtc acc ttt tca gcc gac aag tcc atc acc 288  
 Pro Ser Phe Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr  
 85 90 95

acc gcc tat ttg cag tgg agt agt ctg gag gcc tcg gac acc gcc atg 336  
 Thr Ala Tyr Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met  
 100 105 110

tac tac tgt gcg agc cga aat cac ttt gtt ttc ggg gaa gtt att act 384  
 Tyr Tyr Cys Ala Ser Arg Asn His Phe Val Phe Gly Glu Val Ile Thr  
 115 120 125

act ttg acg gct ggg gcc agg gaa acc ctg ggt cac cgt ctc c 427  
 Thr Leu Thr Ala Gly Ala Arg Glu Thr Leu Gly His Arg Leu  
 130 135 140

<210> 4

<211> 402

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)...(402)

<400> 4

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 Leu Gly Leu Arg Trp Val Phe Leu Val Ala Phe Leu Glu Gly Val Gln  
 1 5 10 15

tgt gag gta cag ctg gtg gag tct ggg gga ggc ttg gta cag cct ggg 96  
 Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly  
 20 25 30

ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc agt agg 144  
 Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg  
 35 40 45

agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg ggg tgg 192  
 Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp  
 50 55 60

ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg gac tca 240

32

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cct ggg ggg tcc ttg aca ctc tcc tgt gca gcc tct gga ttc acc ttc      144
Pro Gly Gly Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      35              40              45

agt agg agt ggc atg cac tgg gtc cgc cag gct cca ggg aag gga ctg      192
Ser Arg Ser Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      50              55              60

gag tgg ctt gca tac att gat tat ggc agt att ttc ata tac tac tcg      240
Glu Trp Leu Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser
      65              70              75              80

gac tca gtg aag ggc cgc ttc acc atc tcc aga gac aac gcc aag aat      288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
      85              90              95

tca ctc tat ctg caa atg aac agc ctg aga gcc gac gac acg gct ttt      336
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe
      100             105             110

tat tac tgt acg acc cat aat tgg ggg gag tta act gac tac tgg ggc      384
Tyr Tyr Cys Thr Thr His Asn Trp Gly Glu Leu Thr Asp Tyr Trp Gly
      115             120             125

cag gga acc ctg gtc acc gtc tcc      408
Gln Gly Thr Leu Val Thr Val Ser
      130             135

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&lt;210&gt; 6

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(421)

&lt;400&gt; 6

atg atg ggg tca acc gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa	48
Met Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln	
1 5 10 15	
gga gtc tgt gca gag gtg cag ctg gtg cag tct gga gca gag gtg aaa	96
Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys	
20 25 30	
aag ccc ggg gag tct ctg aag atc tcc tgt aag ggc tct gga tac agt	144
Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser	
35 40 45	
ttt acc aac tac tgg atg ggc tgg gtg tgc cag atg ccc ggg aaa ggc	192
Phe Thr Asn Tyr Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly	
50 55 60	
ccg gag tgc atg ggg atc atc tat cct gat gac tct gat acc aga tac	240
Pro Glu Cys Met Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr	
65 70 75 80	
agc ccg tcc ttc caa ggc cag gtc acc atc tca gcc gac aag tcc atc	288
Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile	
85 90 95	
agc acc gcc tac cta caa tgg agc aac ctg aag gcc tcg gac acc gcc	336
Ser Thr Ala Tyr Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala	
100 105 110	
ata tat tac tgt gcg aga tgt tat ggt tgg act act tgc gaa gct ttt	384
Ile Tyr Tyr Cys Ala Arg Cys Tyr Gly Trp Thr Thr Cys Glu Ala Phe	
115 120 125	
gat atc tgg ggc caa ggg aca atg gtc acc gtc tct t	421
Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser	

130

135

140

&lt;210&gt; 7

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(417)

&lt;400&gt; 7

ttg tgg ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc	48
Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser	
1                      5                      10                      15	
cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag	96
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln	
20                      25                      30	
acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt	144
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly	
35                      40                      45	
agt tac tac tgg agt tgg atc cgg cag ccc gcc ggg aag cga ctg gag	192
Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu	
50                      55                      60	
tgg att ggg tat att tat tat agt ggg agt acc tac tac aac cca tcc	240
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser	
65                      70                      75                      80	
ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc	288
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe	
85                      90                      95	

tcc ctg aag ctg agc tct gtg acc gcc gca gac acg gcc gtc tat tac 336  
 Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 100 105 110

tgt gcg aga tct ccc caa aac gta tta caa tct ttg gac tgc ttc gac 384  
 Cys Ala Arg Ser Pro Gln Asn Val Leu Gln Ser Leu Asp Cys Phe Asp  
 115 120 125

ccc tgg ggc cag gga acc ctg gtc acc gtc tcc 417  
 Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 130 135

<210> 8  
 <211> 369  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(369)

<400> 8

gtc cag tcc cag gtc cag ctg gtg cag tcc ggg gct gag gtg aag aag 48  
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 1 5 10 15

cct ggg tcc tca gtg aag gtc tcc tgc aag gtt tcc gga ggc acc ttc 96  
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Val Ser Gly Gly Thr Phe  
 20 25 30

agc acc tat ggt ttc agc tgg gtg cgg cag gcc cct gga caa ggg ctt 144  
 Ser Thr Tyr Gly Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 35 40 45

gag tgg atg gga atg atc atc cct atc gtt ggc aca gta aag tac gca 192  
 Glu Trp Met Gly Met Ile Ile Pro Ile Val Gly Thr Val Lys Tyr Ala

50

55

60

cag agg ttc cag ggc aga gtc tca att aat gcg gac aca tcc acg aat 240  
 Gln Arg Phe Gln Gly Arg Val Ser Ile Asn Ala Asp Thr Ser Thr Asn  
 65 70 75 80

ata gcc tac atg gag ctg acc agc ctg aga tct gag gac acg gcc gtc 288  
 Ile Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val  
 85 90 95

tat tac tgt gcg aca gat ctg acg gtg act act aat gat gca ttt gat 336  
 Tyr Tyr Cys Ala Thr Asp Leu Thr Val Thr Thr Asn Asp Ala Phe Asp  
 100 105 110

atc tgg ggc caa ggg aca atg gtc acc gtc tct 369  
 Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser  
 115 120

&lt;210&gt; 9

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(423)

&lt;400&gt; 9

atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt 48  
 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly  
 1 5 10 15

gtc cag tgt gag gtg cag ctg gtg gag tct ggg gaa ggc ttg gta aag 96  
 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Glu Gly Leu Val Lys  
 20 25 30

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cct ggg ggt tcc ctg aga ctc tcg tgt gca gcc tct gga ttc acc ttc      144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
      35              40              45

agt agt ttt ctt atg ttc tgg gtc cgc cag gct cca gaa aag ggg ctg      192
Ser Ser Phe Leu Met Phe Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
      50              55              60

gag tgg gtc tca act att gat gtt agt ggt ggt aat atg tgg tac cga      240
Glu Trp Val Ser Thr Ile Asp Val Ser Gly Gly Asn Met Trp Tyr Arg
      65              70              75              80

gac tct gtc aag ggc cga ttc acc atg tcc aga gac aat tcc aag aac      288
Asp Ser Val Lys Gly Arg Phe Thr Met Ser Arg Asp Asn Ser Lys Asn
      85              90              95

aca ctg tat ctg caa atg acc agc ctg aga gcc gac gac acg gcc gtt      336
Thr Leu Tyr Leu Gln Met Thr Ser Leu Arg Ala Asp Asp Thr Ala Val
      100             105             110

tac tat tgt gcg aga gag gga cga gac cct agc ggc act tgg gga tac      384
Tyr Tyr Cys Ala Arg Glu Gly Arg Asp Pro Ser Gly Thr Trp Gly Tyr
      115             120             125

ttt gac tac tgg ggc cag gga atc ctg gtc acc gtc tcc      423
Phe Asp Tyr Trp Gly Gln Gly Ile Leu Val Thr Val Ser
      130             135             140

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&lt;210&gt; 10

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 10

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1                      5                      10                      15  
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Thr Ser Ala  
                     20                      25                      30  
 Tyr Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu  
                     35                      40                      45  
 Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Thr Ile Phe Ser Asn Pro Ser  
                     50                      55                      60  
 Leu Lys Ser Arg Val Ala Met Ser Val Gly Thr Ser Lys Thr Gln Phe  
 65                      70                      75                      80  
 Ser Leu Ser Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
                     85                      90                      95  
 Cys

&lt;210&gt; 11

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 11

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Gly Val Ser Gly Ala Ser Ile Asn Ser Gly  
 20 25 30  
 Val His Tyr Trp Ala Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu  
 35 40 45  
 Trp Ile Gly Asn Ile Tyr His Ser Gly Ser Ala Tyr Tyr Thr Pro Ser  
 50 55 60  
 Leu Glu Ser Arg Val Ser Met Ser Ile Glu Thr Ser Lys Ser Gln Phe  
 65 70 75 80  
 Phe Leu Asn Leu Asn Ser Leu Thr Ala Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

<210> 12  
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 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 12

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr  
 20 25 30  
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr

65                                70                                75                                80  
 Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
                               85                                90                                95

<210> 13  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 13

Asp Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1                                5                                10                                15  
 Ser Leu Lys Ile Ser Cys Lys Val Ser Gly Asn Glu Phe Thr Asn Tyr  
                               20                                25                                30  
 Trp Ile Ala Trp Val Arg Gln Met Ser Gly Lys Gly Leu Glu Trp Met  
                               35                                40                                45  
 Gly Ser Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Asn Pro Ser Phe  
                               50                                55                                60  
 Gln Gly Gln Val Thr Phe Ser Ala Asp Lys Ser Ile Thr Thr Ala Tyr  
 65                                70                                75                                80  
 Leu Gln Trp Ser Ser Leu Glu Ala Ser Asp Thr Ala Met Tyr Tyr Cys  
                               85                                90                                95

<210> 14  
 <211> 96  
 <212> PRT  
 <213> Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 14

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Thr Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Ser  
 20 25 30  
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Gly Trp Leu  
 35 40 45  
 Ala Tyr Ile Asp Tyr Gly Ser Ile Phe Ile Tyr Tyr Ser Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Phe Tyr Tyr Cys  
 85 90 95

&lt;210&gt; 15

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 15

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu  
 1 5 10 15  
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Asn Tyr  
 20 25 30  
 Trp Met Gly Trp Val Cys Gln Met Pro Gly Lys Gly Pro Glu Cys Met  
 35 40 45  
 Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe  
 50 55 60  
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Trp Ser Asn Leu Lys Ala Ser Asp Thr Ala Ile Tyr Tyr Cys  
 85 90 95

&lt;210&gt; 16

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(37)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (52)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 16

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln  
 1 5 10 15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly  
 20 25 30  
 Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Arg Leu Glu  
 35 40 45  
 Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser  
 50 55 60



<213> Pan troglodytes

<223> CDRI

<223> CDR II

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Glu	Gly	Leu	Val	Lys	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Phe
			20					25					30		
Leu	Met	Phe	Trp	Val	Arg	Gln	Ala	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Thr	Ile	Asp	Val	Ser	Gly	Gly	Asn	Met	Trp	Tyr	Arg	Asp	Ser	Val
	50					55				60					
Lys	Gly	Arg	Phe	Thr	Met	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	
Leu	Gln	Met	Thr	Ser	Leu	Arg	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

<213> Pan troglodytes

 $\langle 222 \rangle \quad (1) \dots (381)$ 

atg agg gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca

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Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Ser
 1              5              10              15

ggt gcc aga tgt gac atc cag atg acc cag ttt cca tcc tcc ctg tct      96
Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser
              20              25              30

gca tct gta gga gac aga gtc acc atc act tgc cag tca agt cag agc      144
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser
              35              40              45

att tac aac tgc ttg agt tgg tat cag cag aaa cca ggg aag gcc cct      192
Ile Tyr Asn Cys Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
              50              55              60

aca ctc cta atc tat ggt gca ttc acc ttg aat agt ggg gtc cca tca      240
Thr Leu Leu Ile Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser
              65              70              75              80

aga ttc agt ggc agt gga tct ggc aca gat ttc act ctc acc atc agc      288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
              85              90              95

aat ctg caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac      336
Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr
              100              105              110

ggc aca cag ctc act ttc ggt gga ggg acc aag gtg gag atc aag      381
Gly Thr Gln Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
              115              120              125

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&lt;210&gt; 20

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

<222> (1) ... (384)

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
1 5 10 15

ctc cca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96  
Leu Pro Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gcc agt 144  
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
35 40 45

cag ggc att agc aat tat tta gcc tgg tat cag cag aaa cca ggg aaa 192  
Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
50 55 60

gcc cct aag ctc ctc atc tat tat gca tcc aga ttg gaa agt ggg gtc 240  
Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val  
65 70 75 80

cca tca agg ttc agc ggc agt gga tct ggg acg gat tac act ctc acc 288  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr  
85 90 95

atc agc agc ctg cag cct gaa gat ttt gca act tat tac tgt caa cag 336  
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110

tat aac agt aac ccc ttt tcg gtg gag gga cca agg tgg aga tca aac 384  
Tyr Asn Ser Asn Pro Phe Ser Val Glu Gly Pro Arg Trp Arg Ser Asn  
115 120 125

<210> 21  
 <211> 384  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 21

atg tcg cca tca caa ctc att ggg ttt ctg ctg ctc tgg gtt cca gcc 48  
 Met Ser Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala  
 1 5 10 15

tcc agg ggt gaa att gtg ctg act cag tct cca gac ttt cag tct gtg 96  
 Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val  
 20 25 30

cct cca aag gag aaa gtc acc atc acc tgc cgg gcc agt cag agc att 144  
 Pro Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile  
 35 40 45

ggc agt agc tta cac tgg tac cag cag aaa cca ggt cag tct cca aag 192  
 Gly Ser Ser Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 50 55 60

ctc ctc atc aag tat gct tcc cag tcc atc tca ggg gtc ccc tcg agg 240  
 Leu Leu Ile Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg  
 65 70 75 80

ttc agt ggc agt gga tct ggg aca gat ttc acc ctc acc atc aat agc 288  
 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser  
 85 90 95

ctg gaa gct gaa gat gct gca acg tat tac tgt cag caa agt agt aat 336  
 Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Asn

100

105

110

tta cct cat acg ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 384  
 Leu Pro His Thr Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
 115 120 125

&lt;210&gt; 22

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 22

gtc cct gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc tca ggt gcc 48  
 Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Ser Gly Ala  
 1 5 10 15

aga tgt gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct 96  
 Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser  
 20 25 30

gta gga gac aga gtc acc atc act tgc cag gca agt cag agc att agc 144  
 Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser  
 35 40 45

aac tat ttg agt tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc 192  
 Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu  
 50 55 60

ctg atc tat gat gca tcc act ttg caa agt ggg gtc cca tca agg ttc 240  
 Leu Ile Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe  
 65 70 75 80

agt ggc agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg 288  
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
                     85                    90                    95

caa cct gaa gat ttt gca aca tat tac tgt cag cgt ggt tac ggt aca 336  
 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Arg Gly Tyr Gly Thr  
                     100                    105                    110

ctc act ttc ggt gga ggg acc aag gtg gag atc aaa 372  
 Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
                     115                    120

<210> 23  
 <211> 384  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 23  
 atg gaa gcc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca 48  
 Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro  
   1                    5                    10                    15

gat acc acc gga gaa ata gtg ttg acg cag tct cca gcc acc ctg tct 96  
 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser  
                     20                    25                    30

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt 144  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser  
                     35                    40                    45

gtt agc agg tac tta gcc tgg tac cag cag aaa cct ggc cag gct ccc 192  
 Val Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro

50

55

60

agg ctc ctc atc tat ggt gca tcc aac agg gcc act ggc atc cca gcc 240  
 Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala  
 65 70 75 80

agg ttc agt ggc agt ggg tct agg aca gac ttc act ctc acc atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser  
 85 90 95

agc gtg gag cct gaa gat ttt gca gtt tat tac tgt cag cag tat aat 336  
 Ser Val Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn  
 100 105 110

aac cag cct ctg atc gcc ttc ggc caa ggg aca cga ctg gag att aaa 384  
 Asn Gln Pro Leu Ile Ala Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys  
 115 120 125

&lt;210&gt; 24

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(387)

&lt;400&gt; 24

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

ttc cca ggt gcc aaa tgt gac atc cag atg acc cag tct cct tcc acc 96  
 Phe Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr  
 20 25 30

ctg tct gcc tcc ata gga gac aga gtc acc atc act tgt cgg gct agt 144  
 Leu Ser Ala Ser Ile Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
           35                          40                          45

cag ggc atc tat aat tat ttg aat tgg tat cag caa aaa cca ggg aga 192  
 Gln Gly Ile Tyr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg  
           50                          55                          60

gcc cct gga ctc ctc atc ttt ggt gcc agg aat ttg gag act ggg gtc 240  
 Ala Pro Gly Leu Leu Ile Phe Gly Ala Arg Asn Leu Glu Thr Gly Val  
           65                          70                          75                          80

cca tca aca ttc agc ggc agt ggt tcc ggg aca cac ttc act ctc acc 288  
 Pro Ser Thr Phe Ser Gly Ser Gly Ser Gly Thr His Phe Thr Leu Thr  
                                   85                                  90                                  95

atc agc agc ctg cag cct ggt gat ttt gcg act tat tac tgt cag caa 336  
 Ile Ser Ser Leu Gln Pro Gly Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
                                   100                                  105                                  110

tat tat act acc ccg tat act ttt ggc cag ggg acc aag ctg gag atc 384  
 Tyr Tyr Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile  
           115                          120                          125

aaa 387

<210> 25  
 <211> 387  
 <212> DNA  
 <213> Pan troglodytes

<220>  
 <221> CDS  
 <222> (1)...(387)

<400> 25

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgt 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys  
 1 5 10 15  
 ttc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tca 96  
 Phe Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30  
 ctg tct gct tct gta gga gac aga gtc acc atc tct tgt cgg gcg agt 144  
 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser  
 35 40 45  
 ctg gat att agc acc tgg tta gcc tgg tat cag cag aaa cca ggg aaa 192  
 Leu Asp Ile Ser Thr Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60  
 gcc cct aag ccc ctg atc tat gct gca tcc act ttg cca agt ggg gtc 240  
 Ala Pro Lys Pro Leu Ile Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val  
 65 70 75 80  
 cca tcg agg ttc agc ggc agt gga tct ggg aca gat ttc act ctc acc 288  
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 85 90 95  
 atc agc agc ctg cag cct gaa gat tct gca act tat tac tgc cga caa 336  
 Ile Ser Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Arg Gln  
 100 105 110  
 tat aat agt tat ccg ctc act ttc ggt gga ggg acc aag gtg gag atc 384  
 Tyr Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 115 120 125  
 aag 387

&lt;210&gt; 26

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(372)

&lt;400&gt; 26

tct	act	cag	ctc	ctg	ggg	ctc	ctg	ctg	ctc	tgg	ctc	cca	ggt	gcc	aaa	48
Ser	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	Gly	Ala	Lys	
1			5					10					15			

tgt	gac	atc	cag	atg	acc	cag	tct	cct	tcc	acc	ctg	tct	gca	tct	gta	96
Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	
			20					25					30			

gga	gac	aga	gtc	acc	atc	act	tgc	cgg	gcc	agt	cag	ggt	att	agt	agc	144
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	
			35					40					45			

tgg	tta	gcc	tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	192
Trp	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
			50				55					60				

atc	tat	aag	gca	tct	agt	tta	gaa	agt	ggg	gtc	cca	tca	agg	ttc	agc	240
Ile	Tyr	Lys	Ala	Ser	Ser	Leu	Glu	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	
			65				70					75			80	

ggc	agt	gga	tct	ggg	aca	gaa	ttc	act	ctc	acc	atc	agc	agc	ctg	cag	288
Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	
							85				90				95	

cct	gat	gat	ttt	gca	act	tat	tac	tgc	caa	cag	tat	agt	agt	tac	cct	336
Pro	Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Ser	Tyr	Pro	
			100					105						110		

cga	acg	ttc	ggc	caa	ggg	acc	aag	ctg	gaa	atc	aaa					372
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			115					120								

&lt;210&gt; 27

&lt;211&gt; 387

&lt;212&gt; DNA

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(387)

&lt;400&gt; 27

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp

1 5 10 15

ctc tca ggt acc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96

Leu Ser Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

20 25 30

ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt 144

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser

35 40 45

cag agc att agc aac tat ttg agt tgg tat cag cag aaa cca ggg aaa 192

Gln Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys

50 55 60

gcc cct aag ctc ctg atc tat tat gca tcc act ttg caa agt ggg gtc 240

Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val

65 70 75 80

cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ctc acc 288

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

85 90 95

atc agc agt ctg caa cct gaa gat ttt gca act tat tac tgt cag cat 336

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His  
 100 105 110

ggg tac ggt aca cat ccc act ttc ggt gga ggg acc aag gtg gag atc 384  
 Gly Tyr Gly Thr His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 115 120 125

aaa 387

<210> 28  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 28

Asp Ile Gln Met Thr Gln Phe Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Gln Ser Ile Tyr Asn Cys  
 20 25 30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Thr Leu Leu Ile  
 35 40 45  
 Tyr Gly Ala Phe Thr Leu Asn Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 29  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1                    5                    10                    15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr  
                   20                    25                    30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                    40                    45  
 Tyr Tyr Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                    55                    60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65                    70                    75                    80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
                   85

<210> 30  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<223> CDRII

<400> 30

[illegible]

<213> Pan troglodytes

<223> CDRI

<223> CDR II

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15  
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Asn Tyr

```

                20                25                30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35                40                45
Tyr Asp Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
      50                55                60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65                70                75                80
Glu Asp Phe Ala Thr Tyr Tyr Cys
                85

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<210> 32
<211> 88
<212> PRT
<213> Pan troglodytes

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<220>
<221> DOMAIN
<222> (24)...(34)
<223> CDRI

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<221> DOMAIN
<222> (50)...(66)
<223> CDRII

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<400> 32

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
  1                5                10                15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
      20                25                30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
      35                40                45
Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
      50                55                60
Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Glu Pro
      65                70                75                80
Glu Asp Phe Ala Val Tyr Tyr Cys
                85

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<210> 33  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 33

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Ile	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Tyr	Asn	Tyr
			20					25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Arg	Ala	Pro	Gly	Leu	Leu	Ile
			35					40					45		
Phe	Gly	Ala	Arg	Asn	Leu	Glu	Thr	Gly	Val	Pro	Ser	Thr	Phe	Ser	Gly
			50					55				60			
Ser	Gly	Ser	Gly	Thr	His	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65						70				75				80	
Gly	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys								
						85									

<210> 34  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 34

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1                      5                      10                      15  
 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Leu Asp Ile Ser Thr Trp  
                     20                      25                      30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile  
                     35                      40                      45  
 Tyr Ala Ala Ser Thr Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly  
                     50                      55                      60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65                      70                      75                      80  
 Glu Asp Ser Ala Thr Tyr Tyr Cys  
                     85

&lt;210&gt; 35

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly  
 1                      5                      10                      15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp  
                   20                                  25                                  30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                                  40                                  45  
 Tyr Lys Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                                  55                                  60  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65                                  70                                  75                                  80  
 Asp Asp Phe Ala Thr Tyr Tyr Cys  
   85

<210> 36  
 <211> 88  
 <212> PRT  
 <213> Pan troglodytes

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1                                  5                                  10                                  15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr  
                   20                                  25                                  30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
                   35                                  40                                  45  
 Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
                   50                                  55                                  60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65                                  70                                  75                                  80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys

<210> 37  
 <211> 408  
 <212> DNA  
 <213> *Macaca cynomolgus*

<220>  
 <221> CDS  
 <222> (1)...(408)

<400> 37

atg gag ttt gga ctg agc tgg gtt ttc ctt gtc gct att ttc aaa ggt	48
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys Gly	
1 5 10 15	
gtc cag tgt gaa gtg cag ttg gtg gag tct ggg gga ggc ttg gta cag	96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln	
20 25 30	
ccg ggg ggg tcc ctg aga ctc gcc tgt gta ggc tct gga ttc gcc ttc	144
Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe	
35 40 45	
aga aac acc agg atg cac tgg att cga cag act cca gga aag agg ctg	192
Arg Asn Thr Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu	
50 55 60	
gag tgg gtg gcc gac ata aag ttt gat gga agt gat ttt tac tat gta	240
Glu Trp Val Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val	
65 70 75 80	
gac tct gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac	288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn	
85 90 95	
tcc ctc tat ctg gaa atg aac agc ctg aga cct gat gac aca gcc gtc	336

Ser Leu Tyr Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val

100

105

110

tat ttc tgt gtg aga gaa tac aga gat gga ctg gat gtc tgg ggc cgg

384

Tyr Phe Cys Val Arg Glu Tyr Arg Asp Gly Leu Asp Val Trp Gly Arg

115

120

125

gga gtt ctg gtc acc gtc tcc tca

408

Gly Val Leu Val Thr Val Ser Ser

130

135

&lt;210&gt; 38

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(381)

&lt;400&gt; 38

gtg aca gct ccc aga tgg gtc ctg tcc cag gtg caa ttg cag gag tcg

48

Val Thr Ala Pro Arg Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ser

1

5

10

15

ggc cca gga ctg gtg aag cct tcg gag acc ctg tcc ctc act tgt act

96

Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr

20

25

30

gtc tct ggt gac tcc atc acc act gtc ttc tgg agc tgg ctc cgc cag

144

Val Ser Gly Asp Ser Ile Thr Thr Val Phe Trp Ser Trp Leu Arg Gln

35

40

45

tcg cca ggg att ggg ctg gag tgg att ggg aat ttt gct ggt agt act

192

Ser Pro Gly Ile Gly Leu Glu Trp Ile Gly Asn Phe Ala Gly Ser Thr

50

55

60

ccg gaa acg aac tac aat ccc tcc ctc aag aat cga gcc acc att tca 240  
 Pro Glu Thr Asn Tyr Asn Pro Ser Leu Lys Asn Arg Ala Thr Ile Ser  
 65 70 75 80

aaa gac acg ccc acg aat caa ttt ttc ctg agg ctg acg tct gtg acc 288  
 Lys Asp Thr Pro Thr Asn Gln Phe Phe Leu Arg Leu Thr Ser Val Thr  
 85 90 95

gcc gcg gac acg gcc gtc tac ttc tgt gcg aga gga ggg gga gcc ggc 336  
 Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg Gly Gly Gly Ala Gly  
 100 105 110

aac cca ctc act tgg ggc cag gga gtc cag gtc acc gtc tcc tca 381  
 Asn Pro Leu Thr Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser  
 115 120 125

<210> 39  
 <211> 417  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1)...(417)

<400> 39

atg ggg tca act gcc atc ctc gcc ctc ctc ctg gct gtt ctc caa gga 48  
 Met Gly Ser Thr Ala Ile Leu Ala Leu Leu Leu Ala Val Leu Gln Gly  
 1 5 10 15

gtc tgt gcc gag gtg cat ctg gtg cag tct gga gca cag gtg aaa agg 96  
 Val Cys Ala Glu Val His Leu Val Gln Ser Gly Ala Gln Val Lys Arg  
 20 25 30

ccc ggg gaa tct ctg agg atc tcc tgt aag act tct gga tac acc ttt 144

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Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
      35              40              45

acc gac agc tgg atc agc tgg gtg cgc cag atg ccc ggg aaa ggc ctg      192
Thr Asp Ser Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu
      50              55              60

gag tgg atg gga aac atc tat cct ggt gat tct gat tcc aga tac aac      240
Glu Trp Met Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn
      65              70              75              80

ccg tcc ttc caa ggc cgc gtc act atc tca gtc gac aag tcc atc agt      288
Pro Ser Phe Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser
              85              90              95

acc acc tac ctg cag tgg agc agc ctg aag gcc tcg gac act gcc aca      336
Thr Thr Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr
              100              105              110

tat tac tgt gcg aag ata gat agc aac tac tac agc cgg ttc gaa gtc      384
Tyr Tyr Cys Ala Lys Ile Asp Ser Asn Tyr Tyr Ser Arg Phe Glu Val
              115              120              125

tgg ggc ccc gga gtc atg gtc acc gtc tcc tca      417
Trp Gly Pro Gly Val Met Val Thr Val Ser Ser
      130              135

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&lt;210&gt; 40

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(423)

&lt;400&gt; 40

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct cct aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

gtc ctg tcc cag gtg cag ttg cag gag tgc ggc cca gga gtg gtg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys  
 20 25 30

cct tgc gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc ttc 144  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe  
 35 40 45

agt act tac tac tgg aat tgg atc cgc cag ccc cca ggg aag gga ctg 192  
 Ser Thr Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu  
 50 55 60

gag tgg att gga tat atc ggt ggt ggt ggt ggt cgc ccc aac tac aat 240  
 Glu Trp Ile Gly Tyr Ile Gly Gly Gly Gly Gly Arg Pro Asn Tyr Asn  
 65 70 75 80

tcc tcc ctc aag agt cgc atc acc ctg tca cta gac gcg tcc aag aac 288  
 Ser Ser Leu Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn  
 85 90 95

cag ttc tcc ctg aac ctg agc tct gtg acc gcc gcg gac acg gcc gtg 336  
 Gln Phe Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val  
 100 105 110

tac tac tgt gcc aga gat cgg ggc tac ggt gcc agc aat gat gct ttt 384  
 Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Gly Ala Ser Asn Asp Ala Phe  
 115 120 125

gat ttc tgg ggc caa ggg ctc agg gtc acc gtc tct tca 423  
 Asp Phe Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser  
 130 135 140

<210> 41  
 <211> 411  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1)...(411)

<400> 41

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca act cct aaa tgg	48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Thr Pro Lys Trp	
1 5 10 15	
gtc ctg tcc cag gtg cag ttg cat gag tcg ggc cct gga ctg ctg aag	96
Val Leu Ser Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys	
20 25 30	
cct tcg gag acc ctg tcc ctc acc tgc aat gtc tcc ggt gac tcc ccc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro	
35 40 45	
act aag tcc acg tgg aac tgg gtc cgc cag tcc cca ggg aag cca ctg	192
Thr Lys Ser Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu	
50 55 60	
gaa tgg att ggt cat gtc ggt tct ggt gga ggt ggc ccc gtt tac aac	240
Glu Trp Ile Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn	
65 70 75 80	
gtc ttc ttg acg ggt cgc gtc tcc atg tct cta gac gct tca aag aag	288
Val Phe Leu Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys	
85 90 95	
ctt ctc tcc ctg gcc tta gca tct gtg acc gcc gcc gac tcg gcc gtc	336
Leu Leu Ser Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val	

100

105

110

tat tac tgt gtc aga tcg acg gca tta ttt tcg ttg gat gtc tgg ggc 384  
 Tyr Tyr Cys Val Arg Ser Thr Ala Leu Phe Ser Leu Asp Val Trp Gly  
 115 120 125

cgg gga ctt ctg gtc acc gtc tcc tca 411  
 Arg Gly Leu Leu Val Thr Val Ser Ser  
 130 135

&lt;210&gt; 42

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(441)

&lt;400&gt; 42

atg gag ttg gga ctg agc tgg gtt ttc ctt ctt gtt gct att tta aaa 48  
 Met Glu Leu Gly Leu Ser Trp Val Phe Leu Leu Val Ala Ile Leu Lys  
 1 5 10 15

ggt gtc cag tgt gac aag cag ctg gtg cag tcg ggg gga ggc ttg gtc 96  
 Gly Val Gln Cys Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val  
 20 25 30

cag cct ggc ggg tct ctg aga ctc gcc tgt gta gcc tcc gga ttc ccc 144  
 Gln Pro Gly Gly Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro  
 35 40 45

ttc agt gac tat tac atg agt tgg gtc cgc cag gct cca ggg aag ggg 192  
 Phe Ser Asp Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly  
 50 55 60

ttg gag tgg ctt gga tta att aaa acc aat cct gat ggt gga acg aca 240  
 Leu Glu Trp Leu Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr  
 65 70 75 80

gat tac gcc gcg tct gtg aaa ggc aga ttt atc atc tca cga gat gat 288  
 Asp Tyr Ala Ala Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp  
 85 90 95

tca aag aac tca ctg ttc ctt caa atg aac agc ctg aaa acc gag gac 336  
 Ser Lys Asn Ser Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp  
 100 105 110

acg gcc gtg tat tac tgc acc aca gaa gtg ttg gtg gtg tct gct att 384  
 Thr Ala Val Tyr Tyr Cys Thr Thr Glu Val Leu Val Val Ser Ala Ile  
 115 120 125

caa ctc att gga tgt ctg ggg ccc ggg gag ttg tgg tca ccc gtc tct 432  
 Gln Leu Ile Gly Cys Leu Gly Pro Gly Glu Leu Trp Ser Pro Val Ser  
 130 135 140

ttc cgc ttc a 442  
 Phe Arg Phe  
 145

<210> 43  
 <211> 407  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1) ... (405)

<400> 43

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1	5	10	15	
gtc ctg tcc cag gtg cag ttg gag gag tcg ggc cca gga ctg gtg aag				96
Val Leu Ser Gln Val Gln Leu Glu Glu Ser Gly Pro Gly Leu Val Lys				
20	25	30		
ccc tcg gag acc ctg tcc ctc acc tgc gct gtg tct ggt ggc ctc att				144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Leu Ile				
35	40	45		
act gga aac tac tgg aac tgg ctc cgg cag tca gaa ggg aag gga ctg				192
Thr Gly Asn Tyr Trp Asn Trp Leu Arg Gln Ser Glu Gly Lys Gly Leu				
50	55	60		
gag tgg att ggc cat att ggt ggt agt agt ggg aac acc ggc tac aac				240
Glu Trp Ile Gly His Ile Gly Gly Ser Ser Gly Asn Thr Gly Tyr Asn				
65	70	75	80	
tcc gct ttc gag agt cgc gtc acc ttg tca aga gac acg gcc aag aat				288
Ser Ala Phe Glu Ser Arg Val Thr Leu Ser Arg Asp Thr Ala Lys Asn				
85	90	95		
cgg ttc tcc ctg aaa ctg acc tct gtg acc gcc gca gat tcg gcc gtc				336
Arg Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Ser Ala Val				
100	105	110		
tat tac tgt gcg aga tcg ggt ttt acc ggc acc gac ttc ttt tac tat				384
Tyr Tyr Cys Ala Arg Ser Gly Phe Thr Gly Thr Asp Phe Phe Tyr Tyr				
115	120	125		
tgg ggc ccg ggg aag tct tgg tc				407
Trp Gly Pro Gly Lys Ser Trp				
130	135			

&lt;210&gt; 44

&lt;211&gt; 420

&lt;212&gt; DNA

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(420)

&lt;400&gt; 44

atg aag cac ctg tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp

1 5 10 15

gtc ctg tcc cag gtt caa cta cag gag tcg ggc cca gga ctg atg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys

20 25 30

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tcc atc 144  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile

35 40 45

agc ggt ggt ttt ggc tgg ggc tgg atc cgt cag tcc ccg ggg aag ggg 192  
 Ser Gly Gly Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly

50 55 60

ctg gaa tgg att gga agt ttc tat act act act gga aat acc ttc tcc 240  
 Leu Glu Trp Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser

65 70 75 80

aac ccc tcc ctc aag agt cga gtc acc att tca gcg gac acg tcc aag 288  
 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys

85 90 95

aac cag ttc tcc ctg aga ctg acc tct gtg acc gcc gcg gac acg gcc 336  
 Asn Gln Phe Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala

100 105 110

gtt tat tac tgt gcg aga gat ctc tat agc agc ggc tat aaa ttt tac 384

Val Tyr Tyr Cys Ala Arg Asp Leu Tyr Ser Ser Gly Tyr Lys Phe Tyr  
 115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 420  
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
 130 135 140

<210> 45  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 45

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ala Cys Val Gly Ser Gly Phe Ala Phe Arg Asn Thr  
 20 25 30  
 Arg Met His Trp Ile Arg Gln Thr Pro Gly Lys Arg Leu Glu Trp Val  
 35 40 45  
 Ala Asp Ile Lys Phe Asp Gly Ser Asp Phe Tyr Tyr Val Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Glu Met Asn Ser Leu Arg Pro Asp Asp Thr Ala Val Tyr Phe Cys  
 85 90 95  
 Val Arg

<210> 46  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

<400> 46

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu  
 1                    5                    10                    15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Thr Thr Val  
                   20                    25                    30  
 Phe Trp Ser Trp Leu Arg Gln Ser Pro Gly Ile Gly Leu Glu Trp Ile  
                   35                    40                    45  
 Gly Asn Phe Ala Gly Ser Thr Pro Glu Thr Asn Tyr Asn Pro Ser Leu  
                   50                    55                    60  
 Lys Asn Arg Ala Thr Ile Ser Lys Asp Thr Pro Thr Asn Gln Phe Phe  
 65                    70                    75                    80  
 Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys  
                   85                    90                    95  
 Ala Arg

<210> 47  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 47

Glu Val His Leu Val Gln Ser Gly Ala Gln Val Lys Arg Pro Gly Glu  
 1 5 10 15  
 Ser Leu Arg Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Asp Ser  
 20 25 30  
 Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 Gly Asn Ile Tyr Pro Gly Asp Ser Asp Ser Arg Tyr Asn Pro Ser Phe  
 50 55 60  
 Gln Gly Arg Val Thr Ile Ser Val Asp Lys Ser Ile Ser Thr Thr Tyr  
 65 70 75 80  
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Thr Tyr Tyr Cys  
 85 90 95  
 Ala Lys

&lt;210&gt; 48

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 48

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys Pro Ser Glu  
 1                    5                    10                    15  
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr  
                   20                    25                    30  
 Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile  
                   35                    40                    45  
 Gly Tyr Ile Gly Gly Gly Gly Gly Arg Pro Asn Tyr Asn Ser Ser Leu  
                   50                    55                    60  
 Lys Ser Arg Ile Thr Leu Ser Leu Asp Ala Ser Lys Asn Gln Phe Ser  
 65                    70                    75                    80  
 Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
                   85                    90                    95  
 Ala Arg

&lt;210&gt; 49

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(35)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(66)

&lt;223&gt; CDRII

&lt;400&gt; 49

Gln Val Gln Leu His Glu Ser Gly Pro Gly Leu Leu Lys Pro Ser Glu  
 1                    5                    10                    15  
 Thr Leu Ser Leu Thr Cys Asn Val Ser Gly Asp Ser Pro Thr Lys Ser  
                   20                    25                    30  
 Thr Trp Asn Trp Val Arg Gln Ser Pro Gly Lys Pro Leu Glu Trp Ile

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          35          40          45
Gly His Val Gly Ser Gly Gly Gly Gly Pro Val Tyr Asn Val Phe Leu
   50          55          60
Thr Gly Arg Val Ser Met Ser Leu Asp Ala Ser Lys Lys Leu Leu Ser
   65          70          75          80
Leu Ala Leu Ala Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys
          85          90          95
Val Arg

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<210> 50
<211> 100
<212> PRT
<213> Macaca cynomolgus

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<220>
<221> DOMAIN
<222> (31)...(35)
<223> CDRI

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<221> DOMAIN
<222> (50)...(68)
<223> CDRII

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<400> 50

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Asp Lys Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ala Cys Val Ala Ser Gly Phe Pro Phe Ser Asp Tyr
          20          25          30
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Leu
          35          40          45
Gly Leu Ile Lys Thr Asn Pro Asp Gly Gly Thr Thr Asp Tyr Ala Ala
          50          55          60
Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Lys Asn Ser
   65          70          75          80
Leu Phe Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
          85          90          95

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Tyr Cys Thr Thr

100

<210> 51  
 <211> 98  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (31)...(35)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(66)  
 <223> CDRII

&lt;400&gt; 51

Gln	Val	Gln	Leu	Glu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5				10					15		
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Val	Ser	Gly	Gly	Leu	Ile	Thr	Gly	Asn
			20					25					30		
Tyr	Trp	Asn	Trp	Leu	Arg	Gln	Ser	Glu	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35				40						45			
Gly	His	Ile	Gly	Gly	Ser	Ser	Gly	Asn	Thr	Gly	Tyr	Asn	Ser	Ala	Phe
	50					55				60					
Glu	Ser	Arg	Val	Thr	Leu	Ser	Arg	Asp	Thr	Ala	Lys	Asn	Arg	Phe	Ser
65				70				75					80		
Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85				90					95		
Ala	Arg														

<210> 52  
 <211> 99  
 <212> PRT  
 <213> Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (31)...(36)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (51)...(67)

&lt;223&gt; CDRII

&lt;400&gt; 52

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Met Lys Pro Ser Glu  
 1                      5                      10                      15  
 Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Gly Gly  
                     20                      25                      30  
 Phe Gly Trp Gly Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp  
                     35                      40                      45  
 Ile Gly Ser Phe Tyr Thr Thr Thr Gly Asn Thr Phe Ser Asn Pro Ser  
                     50                      55                      60  
 Leu Lys Ser Arg Val Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe  
 65                      70                      75                      80  
 Ser Leu Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
                     85                      90                      95  
 Cys Ala Arg

&lt;210&gt; 53

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 53

atg gac ata agg gtc ccc gtg cag ctc ctg ggg ctc ctg ttg ctc tgg

48

Met Asp Ile Arg Val Pro Val Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15  
 ctc cga ggt gcc aga tgt gac atc cag atg acc cag tct cca tcc tcc 96  
 Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30  
 ctg tct aca tct gta gga gac act gtc acc atc act tgc cgg gcg agt 144  
 Leu Ser Thr Ser Val Gly Asp Thr Val Thr Ile Thr Cys Arg Ala Ser  
 35 40 45  
 caa ggc att gac acg gag tta gcc tgg tat cag cag aaa cca ggt aaa 192  
 Gln Gly Ile Asp Thr Glu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys  
 50 55 60  
 gcc ccc aca ctc ctg atc tct gat gcc tcc agg ttg cag acg ggg gtc 240  
 Ala Pro Thr Leu Leu Ile Ser Asp Ala Ser Arg Leu Gln Thr Gly Val  
 65 70 75 80  
 tca tct cgg ttc agc ggc agt gga tct gga aca gat ttc act ctc acc 288  
 Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 85 90 95  
 atc aac agc ctg cag cct gaa gat att gcg act tat tac tgt caa cag 336  
 Ile Asn Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln  
 100 105 110  
 gat aat agt ttt cca ctc act ttc ggc gga ggg acc aag gtg gag atc 384  
 Asp Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
 115 120 125  
 aaa cga 390  
 Lys Arg  
 130

&lt;210&gt; 54

&lt;211&gt; 384

&lt;212&gt; DNA

<213> *Macaca cynomolgus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(384)

&lt;400&gt; 54

gtc ttc att tcc ctg ttg ctc tgg atc tct ggt gcc tgt ggg gac att	48
Val Phe Ile Ser Leu Leu Leu Trp Ile Ser Gly Ala Cys Gly Asp Ile	
1 5 10 15	
gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agg	96
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg	
20 25 30	
gtc acc atc aat tgt aag tcc agc cag agt ctt tta tac agc tcc aac	144
Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn	
35 40 45	
aat aag aac tac tta gcc tgg tac cag caa aaa cca gga cag gct cct	192
Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro	
50 55 60	
caa cta ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc cct aat	240
Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asn	
65 70 75 80	
cga ttt agt ggc agc ggc tct ggg aca gat ttc act ctc acc atc agt	288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser	
85 90 95	
ggc ctg cag gct gaa gat gtg gca gtg tat tac tgt caa cag tat tat	336
Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr	
100 105 110	

gat atg ccc gac agt ttt ggc cag ggg acc aaa gtg gac atc aaa cga 384  
 Asp Met Pro Asp Ser Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg  
 115 120 125

<210> 55

<211> 399

<212> DNA

<213> Macaca cynomolgus

<220>

<221> CDS

<222> (1)...(399)

<400> 55

atg agg ctc cct gct cag ctc ctg ggg ctg cta ttg ctc tgc gtc ccc 48  
 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro  
 1 5 10 15

gga tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96  
 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
 20 25 30

gtc atc cct gga cag cca gcc tcc atc tcc tgc agg tct agt caa agc 144  
 Val Ile Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 35 40 45

ctt gta cat agt gac ggg aaa acc tac ttg aat tgg tta caa cag aag 192  
 Leu Val His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys  
 50 55 60

cca ggc caa cct cca aga ctc ctg att tat cag gtt tct aac cgg cac 240  
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His  
 65 70 75 80

tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gac ttc 288  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe

85

90

95

aca ctg aaa atc agc aga gtg gag act gag gat gtt ggg gtt tat tcc 336  
 Thr Leu Lys Ile Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser  
 100 105 110

tgc gtg caa ggt aca cac tgg ccg tgg acg ttc ggc caa ggg acc aag 384  
 Cys Val Gln Gly Thr His Trp Pro Trp Thr Phe Gly Gln Gly Thr Lys  
 115 120 125

gtg gac atc aaa cga 399  
 Val Asp Ile Lys Arg  
 130

<210> 56  
 <211> 384  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1)...(384)

<400> 56

atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg ctc cca 48  
 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro  
 1 5 10 15

ggc gcc ata tgt gac att cag atg tcc cag tct cca tcc tcc ctg tct 96  
 Gly Ala Ile Cys Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser  
 20 25 30

gct tct gtg gga gac aga gtc acc atc acc tgc cgg gca agt cag ggc 144  
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly  
 35 40 45

ata act aat tat tta aac tgg tat cag cag aaa ccg ggg aaa gcc cct 192  
 Ile Thr Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro  
 50 55 60

aac ctc ctg atc tat tat gca act cgt ttg gcg agc ggg gtc cca tca 240  
 Asn Leu Leu Ile Tyr Tyr Ala Thr Arg Leu Ala Ser Gly Val Pro Ser  
 65 70 75 80

agg ttc agc ggc agt gga tct ggg tcg gag tac agt ctc gcc atc agc 288  
 Arg Phe Ser Gly Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser  
 85 90 95

agc ctg cag cct gaa gat ttt gca acc tat ttc tgt caa cag ggt tat 336  
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Tyr  
 100 105 110

agg gcc ccc tac act ttt ggc cag ggg acc aca gtg gag atc aaa cga 384  
 Arg Ala Pro Tyr Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg  
 115 120 125

<210> 57  
 <211> 390  
 <212> DNA  
 <213> Macaca cynomolgus

<220>  
 <221> CDS  
 <222> (1)...(390)

<400> 57

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctg ctg ctc tgg 48  
 Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp  
 1 5 10 15

ctc cta ggt gcc aga tgt gac atc cag atg acc cag tct cct tct tcc 96  
 Leu Leu Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

20	25	30	
ttg tct gca tct gta gga gac aga gtc acc atc act tgc caa gcc agt			144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser			
35	40	45	
cag ggt att agc aac tgg tta gcc tgg tat cag cag aaa ccg ggg aaa			192
Gln Gly Ile Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys			
50	55	60	
gcc cct aag ctc ctg atc tat gct gca tcc act ttc caa agt ggg gtc			240
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val			
65	70	75	80
cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc			288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr			
85	90	95	
atc agc agc ctg cag cct gaa gat ttt gca act tac tac tgt caa cag			336
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln			
100	105	110	
tat aat act tac cct ctc act ttc ggc gga ggg acc aag gtg gag atc			384
Tyr Asn Thr Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile			
115	120	125	
aaa cga			390
Lys Arg			
130			

&lt;210&gt; 58

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(390)

&lt;400&gt; 58

atg gac ttg agg gcc ccc gct cat ctc cta ggg ctc ctg ctg ctc tgg	48
Met Asp Leu Arg Ala Pro Ala His Leu Leu Gly Leu Leu Leu Leu Trp	
1 5 10 15	
ctc cca ggt gcc aga ggt gac atc cag atg acc cag tct cca ccc tcc	96
Leu Pro Gly Ala Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Pro Ser	
20 25 30	
ctg tct gcg tct gtt ggg gac act gtc agt ctt act tgt cgg gca agt	144
Leu Ser Ala Ser Val Gly Asp Thr Val Ser Leu Thr Cys Arg Ala Ser	
35 40 45	
cag cct att ggc agt aat tta aat tgg ttc cag caa aaa cct ggg agc	192
Gln Pro Ile Gly Ser Asn Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser	
50 55 60	
ccc ccc aga ctc ctg atc tac ctt gcg acc gcc ttg caa cgt ggg atc	240
Pro Pro Arg Leu Leu Ile Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile	
65 70 75 80	
ccg tca agg ttt agc gcc act gga tct caa acc aat ttc act ctc acg	288
Pro Ser Arg Phe Ser Ala Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr	
85 90 95	
atc acc ggc ctg cag cct gag gat ttc gca act tac ctc tgt ctg caa	336
Ile Thr Gly Leu Gln Pro Glu Asp Phe Ala Thr Tyr Leu Cys Leu Gln	
100 105 110	
cat act tct tac cca ttc act ttt ggc ccc ggg aca aag gtg gat atc	384
His Thr Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile	
115 120 125	
aag cga	390

Lys Arg

130

<210> 59  
 <211> 88  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(56)  
 <223> CDRII

<400> 59

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Thr	Ser	Val	Gly
1				5				10					15		
Asp	Thr	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Asp	Thr	Glu
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Thr	Leu	Leu	Ile
			35					40					45		
Ser	Asp	Ala	Ser	Arg	Leu	Gln	Thr	Gly	Val	Ser	Ser	Arg	Phe	Ser	Gly
			50					55					60		
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Ser	Leu	Gln	Pro
65								70					75		80
Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys								

<210> 60  
 <211> 94  
 <212> PRT  
 <213> Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(40)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (56)...(62)

&lt;223&gt; CDRII

&lt;400&gt; 60

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1             5             10             15
Glu Arg Val Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
      20             25             30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
      35             40             45
Ala Pro Gln Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
      50             55             60
Pro Asn Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
      65             70             75             80
Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
      85             90

```

&lt;210&gt; 61

&lt;211&gt; 93

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(39)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (54)...(61)

&lt;223&gt; CDRII

&lt;400&gt; 61

```

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ile Pro Gly
 1             5             10             15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
      20             25             30
Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Lys Pro Gly Gln Pro
      35             40             45
Pro Arg Leu Leu Ile Tyr Gln Val Ser Asn Arg His Ser Gly Val Pro
      50             55             60
Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65             70             75             80
Ser Arg Val Glu Thr Glu Asp Val Gly Val Tyr Ser Cys
      85             90

```

&lt;210&gt; 62

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 62

```

Asp Ile Gln Met Ser Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Asn Tyr
      20             25             30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
      35             40             45
Tyr Tyr Ala Thr Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
      50             55             60

```

Ser Gly Ser Gly Ser Glu Tyr Ser Leu Ala Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Phe Cys  
 85

<210> 63  
 <211> 88  
 <212> PRT  
 <213> Macaca cynomolgus

<220>  
 <221> DOMAIN  
 <222> (24)...(34)  
 <223> CDRI

<221> DOMAIN  
 <222> (50)...(56)  
 <223> CDRII

<400> 63

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15  
 Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Gly Ile Ser Asn Trp  
 20 25 30  
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 Tyr Ala Ala Ser Thr Phe Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys  
 85

<210> 64  
 <211> 88  
 <212> PRT  
 <213> Macaca cynomolgus

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (24)...(34)

&lt;223&gt; CDRI

&lt;221&gt; DOMAIN

&lt;222&gt; (50)...(56)

&lt;223&gt; CDRII

&lt;400&gt; 64

```

Asp Ile Gln Met Thr Gln Ser Pro Pro Ser Leu Ser Ala Ser Val Gly
 1               5               10               15
Asp Thr Val Ser Leu Thr Cys Arg Ala Ser Gln Pro Ile Gly Ser Asn
          20               25               30
Leu Asn Trp Phe Gln Gln Lys Pro Gly Ser Pro Pro Arg Leu Leu Ile
          35               40               45
Tyr Leu Ala Thr Ala Leu Gln Arg Gly Ile Pro Ser Arg Phe Ser Ala
          50               55               60
Thr Gly Ser Gln Thr Asn Phe Thr Leu Thr Ile Thr Gly Leu Gln Pro
65               70               75               80
Glu Asp Phe Ala Thr Tyr Leu Cys
          85

```

&lt;210&gt; 65

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 65

```

gac acg gtg ctg acc cag tct cct gct ttg gct gtg cct cca gga gag
Asp Thr Val Leu Thr Gln Ser Pro Ala Leu Ala Val Pro Pro Gly Glu
 1               5               10               15

```

48

agg gtt acc gtc tcc tgt agg gcc agt gaa agt gtc agt aca ttt ttg	96
Arg Val Thr Val Ser Cys Arg Ala Ser Glu Ser Val Ser Thr Phe Leu	
20 25 30	
 cac tgg tat caa cag aaa cca gga cat caa ccc aaa ctc ctc atc tat	144
His Trp Tyr Gln Gln Lys Pro Gly His Gln Pro Lys Leu Leu Ile Tyr	
35 40 45	
 cta gcc tca aaa cta gaa tct ggg gtc cct gcc agg ttc agt ggc ggt	192
Leu Ala Ser Lys Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly Gly	
50 55 60	
 ggg tct ggg aca gac ttc acc ctc acc att gat cct gtg gag gct gat	240
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asp Pro Val Glu Ala Asp	
65 70 75 80	
 gac act gct acc tat tac tgt cag cag acc tgg aat gat cct cgg acg	288
Asp Thr Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg Thr	
85 90 95	
 ttc ggt gga ggc acc aag ctg gaa ttg aaa cgg gct gat gct gca cca	336
Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro	
100 105 110	
 act gta tct atc ttc cca cca tcc	360
Thr Val Ser Ile Phe Pro Pro Ser	
115 120	

&lt;210&gt; 66

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 66

gag gtc cag ctg cag cag tct gga cct gag gtt ggg agg cct ggg tcc	48
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Val Gly Arg Pro Gly Ser	
1 5 10 15	
tca gtc aag att tct tgc aag gct tct ggc tac acc ttt aca gat tac	96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr	
20 25 30	
gtt ttg aat tgg gtg aag cag agt cct gga cag gga ctg gaa tgg ata	144
Val Leu Asn Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga tgg att gat cct gac tat ggt act act gat tat gct gag aag ttc	192
Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe	
50 55 60	
aaa aag aag gcc aca ctg act gca gat aca tcc tcc agc aca gcc tac	240
Lys Lys Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
atc cag ctt agc agc ctg aca tct gag gac aca gcc acc tat ttt tgt	288
Ile Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Thr Tyr Phe Cys	
85 90 95	
gct aga tct agg aat tac gga gga tat att aat tac tgg ggc caa gga	336
Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly	
100 105 110	
gtc atg gtc aca gtc tcc tca gct	360
Val Met Val Thr Val Ser Ser Ala	
115 120	

&lt;210&gt; 67

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 67

Ala	Val	His	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		
Asp	Ser	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Asn	Ile	Tyr
			20					25					30		
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
			35					40					45		
Phe	Asp	Ala	Ser	Ile	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
			50					55					60		
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Ser	Leu	Thr	Ile	Arg	Ser	Leu	Gln	Pro
			65					70					75		80
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Cys	Gly	Trp	Gly	Thr	His	Pro
								85					90		95
Tyr	Asn	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg			
								100					105		

&lt;210&gt; 68

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; rat/chimpanzee sequence

&lt;400&gt; 68

Asp	Thr	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		
Asp	Ser	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Glu	Ser	Val	Ser	Thr	Phe
			20					25					30		
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
			35					40					45		
Tyr	Leu	Ala	Ser	Lys	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly
			50					55					60		

Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Arg Ser Leu Gln Pro  
 65                                70                                75                                80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Trp Asn Asp Pro Arg  
                               85                                90                                95  
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg  
                               100                                105

<210> 69  
 <211> 128  
 <212> PRT  
 <213> Pan troglodytes

<400> 69  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
   1                                5                                10                                15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Phe  
                               20                                25                                30  
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
                               35                                40                                45  
 Ser Leu Val Ser Trp Asp Ser Tyr Asn Ile Tyr His Ala Asp Ser Val  
                               50                                55                                60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Ser Leu Tyr  
   65                                70                                75                                80  
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys  
                               85                                90                                95  
 Ala Lys Ala Asp Thr Gly Gly Asp Phe Asp Tyr Val Ser Asp Ser Trp  
                               100                                105                                110  
 Arg Cys Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
                               115                                120                                125

<210> 70  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> rat/chimpanzee sequence

&lt;400&gt; 70

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30  
 Val Leu Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Trp Ile Asp Pro Asp Tyr Gly Thr Thr Asp Tyr Ala Glu Lys Phe  
 50 55 60  
 Lys Lys Lys Ala Thr Leu Ser Ala Asp Thr Ser Arg Asn Ser Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Asp Leu Arg Pro Glu Asp Thr Ala Ile Tyr Phe Cys  
 85 90 95  
 Ala Arg Ser Arg Asn Tyr Gly Gly Tyr Ile Asn Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser  
 115

&lt;210&gt; 71

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(354)

&lt;400&gt; 71

caa gtt cag ctt caa cag tct gga gct gag ctg atg aag cct ggg gcc 48  
 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala  
 1 5 10 15  
 tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96  
 Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr  
 20 25 30

tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144  
 Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile  
           35                          40                          45

gga gag att tta cct aga agt ggt aat act aac tac aat gag aag ttc 192  
 Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe  
           50                          55                          60

aag ggc aag gcc aca ttc act gca gaa aca tcc tcc aac aca gcc tac 240  
 Lys Gly Lys Ala Thr Phe Thr Ala Glu Thr Ser Ser Asn Thr Ala Tyr  
           65                          70                          75                          80

atg caa ctc agc agc ctg aca cct gag gac tct gcc gtc tat tac tgt 288  
 Met Gln Leu Ser Ser Leu Thr Pro Glu Asp Ser Ala Val Tyr Tyr Cys  
                                   85                          90                          95

tca agt cgc ggc gtc agg ggc tct atg gac tac tgg ggt caa gga acc 336  
 Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr  
                           100                          105                          110

tca gtc acc gtc tcc tca 354  
 Ser Val Thr Val Ser Ser  
           115

<210> 72  
 <211> 324  
 <212> DNA  
 <213> Murine  
  
 <220>  
 <221> CDS  
 <222> (1)...(324)

<400> 72  
 gat att cag atg acc cag act aca tcc tcc ctg tct gcc tct ctg gga 48  
 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

1	5	10	15	
gac aga gtc acc atc act tgc agg tca agt cag gac att agc aat ttt				96
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe				
20		25	30	
tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc				144
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile				
35		40	45	
tac tac aca tca aca tta cac tca gga gtc cca tca agg ttc agt ggc				192
Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly				
50		55	60	
agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa				240
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln				
65		70	75	80
gaa gat att gcc act tac ttt tgc caa cag ggt aat acg ctt cct tgg				288
Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp				
	85	90	95	
acg ttc ggt gga ggc acc aac ctg gaa atc aaa cgg				324
Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys Arg				
100		105		

&lt;210&gt; 73

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/chimpanzee sequence

&lt;400&gt; 73

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

```

      1             5             10             15
Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Asp Ile Ser Asn Phe
      20             25             30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35             40             45
Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
      50             55             60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
      65             70             75             80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp
      85             90             95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
      100             105

```

&lt;210&gt; 74

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/chimpanzee sequence

&lt;400&gt; 74

```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
      1             5             10             15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
      20             25             30
Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
      35             40             45
Gly Glu Ile Leu Pro Arg Ser Gly Asn Thr Asn Tyr Asn Glu Lys Phe
      50             55             60
Lys Gly Lys Ala Ser Phe Asn Ala Asp Thr Ser Thr Asn Ile Ala Tyr
      65             70             75             80
Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
      85             90             95
Ser Ser Arg Gly Val Arg Gly Ser Met Asp Tyr Trp Gly Gln Gly Thr
      100             105             110

```

Leu Val Thr Val Ser Ser

115

&lt;210&gt; 75

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Murine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(360)

&lt;400&gt; 75

caa gtt cag ctt caa cag cct ggg gct gag ctt gtg aag tct ggg gcc 48

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Ser Gly Ala

1

5

10

15

tca gtg aag ctg tcc tgc aag gct tct ggc agt acc ttc acc agc tac 96

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr

20

25

30

tgg atg cac tgg gtg aag cag agg cct gga cga ggc ctt gag tgg att 144

Trp Met His Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile

35

40

45

gga agg att gat cca aat agt ggt ggt act aag gat aat gag aag ttc 192

Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe

50

55

60

aag agc aag gcc aca ctg act gta gac aaa ccc tcc agc aca gcc tac 240

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Pro Ser Ser Thr Ala Tyr

65

70

75

80

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tat tgt 288

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys

85

90

95

gca aga gag acc tac tat gat tcc tcg ttt gct tac tgg ggc caa ggg 336  
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110

act ctg gtc act gtc tct gca gcc 360  
 Thr Leu Val Thr Val Ser Ala Ala  
 115 120

<210> 76

<211> 336

<212> DNA

<213> Murine

<220>

<221> CDS

<222> (1)...(336)

<400> 76

gat att gtt atg act cag tct caa aaa ttc atg tcc aca tca gta gga 48  
 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
 1 5 10 15

gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96  
 Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

gta gcc tgg tat caa cag aaa cca ggg caa tct cct aaa gca ctg att 144  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile  
 35 40 45

tac tcg gca tcc tac cgg tac agt gga gtc cct gat cgc ttc aca ggc 192  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly  
 50 55 60

agt gga tct ggg aca gat ttc act ctc acc atc agc aat gtg cag tct 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser

acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgg gct gat gct gca 336  
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala  
100 105 110

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<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> murine/chimpanzee sequence
```

```

<400> 77
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1              5              10              15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
      20              25              30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile
      35              40              45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly
      50              55              60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65              70              75              80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu
      85              90              95
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
      100              105

```

<210> 78  
<211> 118

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/chimpanzee sequence

&lt;400&gt; 78

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr  
 20 25 30  
 Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
 35 40 45  
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe  
 50 55 60  
 Lys Ser Lys Ala Thr Leu Asn Val Asp Lys Ser Thr Asn Ile Ala Tyr  
 65 70 75 80  
 Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Met Val Thr Val Ser  
 115

&lt;210&gt; 79

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; murine/human sequence

&lt;400&gt; 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
 1 5 10 15  
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Ser Thr Phe Thr Ser Tyr  
 20 25 30  
 103

Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile  
                   35                  40                  45  
 Gly Arg Ile Asp Pro Asn Ser Gly Gly Thr Lys Asp Asn Glu Lys Phe  
                   50                  55                  60  
 Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr  
                   65                  70                  75                  80  
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                                   85                  90                  95  
 Ala Arg Glu Thr Tyr Tyr Asp Ser Ser Phe Ala Tyr Trp Gly Gln Gly  
                   100                  105                  110  
 Thr Met Val Thr Val Ser Ala  
                   115

<210> 80

<211> 102

<212> PRT

<213> Artificial Sequence

<220>

<223> murine/human sequence

<400> 80

Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
           1                  5                  10                  15  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
                   20                  25                  30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
                   35                  40                  45  
 Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Ser Gly  
                   50                  55                  60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
                   65                  70                  75                  80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Leu  
                                   85                  90                  95  
 Thr Phe Gly Gly Gly Thr  
                   100

<210> 81  
 <211> 11  
 <212> PRT  
 <213> Pan troglodytes

<400> 81  
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser  
 1 5 10

<210> 82  
 <211> 11  
 <212> PRT  
 <213> Pan troglodytes

<400> 82  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 1 5 10

<210> 83  
 <211> 11  
 <212> PRT  
 <213> Pan troglodytes

<400> 83  
 Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser  
 1 5 10

<210> 84  
 <211> 11  
 <212> PRT  
 <213> Pan troglodytes

<400> 84  
 Trp Gly Gln Gly Ile Leu Val Thr Val Ser Ser  
 1 5 10

<210> 85

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 85

Trp Gly Arg Gly Ile Leu Val Ile Val Ser Ser

1

5

10

&lt;210&gt; 86

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 86

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg

1

5

10

&lt;210&gt; 87

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 87

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg

1

5

10

&lt;210&gt; 88

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 88

Trp Gly Arg Gly Val Leu Val Thr Val Ser Ser

1

5

10

&lt;210&gt; 89

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 89

Trp Gly Gln Gly Val Gln Val Thr Val Ser Ser

1 5 10

&lt;210&gt; 90

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 90

Trp Gly Pro Gly Val Met Val Thr Val Ser Ser

1 5 10

&lt;210&gt; 91

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 91

Trp Gly Arg Gly Leu Leu Val Thr Val Ser Ser

1 5 10

&lt;210&gt; 92

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Macaca cynomolgus

&lt;400&gt; 92

Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser

1 5 10

&lt;210&gt; 93

&lt;211&gt; 11

&lt;212&gt; PRT

<213> Macaca cynomolgus

<400> 93

Trp Gly Gln Gly Leu Arg Val Thr Val Ser Ser

1 5 10

<210> 94

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 94

Phe Gly Gln Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

<210> 95

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 95

Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg

1 5 10

<210> 96

<211> 11

<212> PRT

<213> Macaca cynomolgus

<400> 96

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg

1 5 10

<210> 97

<211> 11

<212> PRT

<213> Pan troglodytes

<400> 97

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

1

5

10